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Composition of the oil-slime microbial community as determined by analysis of the 16S rRNA gene

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Abstract

Analysis of the 16S rRNA genes of the cultured microorganisms of industrial oil-slime revealed predominance (~85-90%) of the Gammaproteobacteria in the community of aerobic heterotrophs and specific oil-slime degraders. Relation of the isolated strains with members of the genera Pseudomonas, Stenotrophomonas, and Enterobacter was established. Analysis of the same gene in the total DNA from the oil-slime revealed greater microbial diversity (~20 operative taxonomic units determined by T-RFLP) than in the cultured part of the community, which included ~12 different colony types. Three major restriction fragments were found, with their total area ~50%. These results demonstrated the low morphological and phylogenetic diversity of the oil-slime bacterial community. © 2013 Pleiades Publishing, Ltd.

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Keywords

16S rRNA, bacterial community, industrial oil-slime, T-RFLP